SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Goli, Surya K.
Hillman, Jennifer L.

(ii) TITLE OF THE INVENTION: A NOVEL GLUTATHIONE S-TRANSFERASE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: INCYTE GENOMICS, INC.
  (B) STREET: 3160 Porter Drive
  (C) CITY: Palo Alto
  (D) STATE: CA
  (E) COUNTRY: US
  (F) ZIP: 94304

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER: 09/309,320
  (B) FILING DATE: May 11, 1999
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER: 09 309,320
  (B) FILING DATE: May 11, 1999

  (A) APPLICATION NUMBER: 09 096,571
  (B) FILING DATE: June 12, 1998

  (A) APPLICATION NUMBER: 08 756,771
  (B) FILING DATE: November 26, 1996

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Billings, Lucy J.
  (B) REGISTRATION NUMBER: 36,749
  (C) REFERENCE DOCKET NUMBER: PF-0163 DIV

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 415-855-0555
  (B) TELEFAX: 415-845-4166
  (C) TELEX:

  (2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Ala Arg Pro Lys Leu His Tyr Pro Asn Gly Arg Gly Arg Met
1   5   10   15
Glu Ser Val Arg Trp Val Leu Ala Ala Ala Gly Val Glu Phe Asp Glu
                20   25   30
Glu Phe Leu Glu Thr Lys Glu Gln Leu Tyr Lys Leu Gln Asp Gly Asn
            35   40   45
His Leu Leu Phe Gln Gln Val Pro Met Val Glu Ile Asp Gly Met Lys
        50   55   60
Leu Val Gln Thr Arg Ser Ile Leu His Tyr Ile Ala Asp Lys His Asn
65   70   75   80
Leu Phe Gly Lys Asn Leu Lys Glu Arg Thr Leu Ile Asp Met Tyr Val
                85   90   95
Glu Gly Thr Leu Asp Leu Leu Glu Leu Leu Ile Met His Pro Phe Leu
                100   105   110
Lys Pro Asp Asp Gln Gln Lys Glu Val Val Asn Met Ala Gln Lys Ala
            115   120   125
Ile Ile Arg Tyr Phe Pro Val Phe Glu Lys Ile Leu Arg Gly His Gly
        130   135   140
Gln Ser Phe Leu Val Gly Asn Gln Leu Ser Leu Ala Asp Val Ile Leu
145   150   155   160
Leu Gln Thr Ile Leu Ala Leu Glu Glu Lys Ile Pro Asn Ile Leu Ser
                165   170   175
Ala Phe Pro Phe Leu Gln Glu Tyr Thr Val Lys Leu Ser Asn Ile Pro
                180   185   190
Thr Ile Lys Arg Phe Leu Glu Pro Gly Ser Lys Lys Lys Pro Pro Pro
            195   200   205
Asp Glu Ile Tyr Val Arg Thr Val Tyr Asn Ile Phe Arg Pro
    210   215   220

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 400 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCAGCAA GCCCCAAGCT CCACTATCCT AACGGAAGAG GTCGATGGA TTCTTTGACA   60
TGGGTTTTAG CTGCCGCTGG AGTCGAGTTT GATGAAGAAT TTCTGGAAAC AAAAGAACAG   120
TTGTACAAGT TGCAGGATGG TAACCACCTG CTGTTCCAAC AAGTGCCCAT GGTTGAAATT   180
GACGGGATGA AGTTGGTACA CACCCCGAAGC ATTCTCCACT ACATAGCAGA CAAGCACAAT   240
CTCTTTGGCA AGAACCTCAA CGAGAGAACC CTGATTGACA TGTACGTGGA GGGGACACTG   300
GATCTGCTGG AACTGCTTAT CATGCATCCT TTCTTAAAAC CAGATGATCA GCAAAAGGAA   360
GTGGTTAACA TGGCCCAGAA GGCTATAAT AATATACTTT CTGGGTTGA AAAGATTTTA   420
AGGGGTCAC GAGTAAAGCTT TGTTCTTGCT AATCAGTTCA GCTTTGAAG TGTGATTTTA   480

TACAGTCATG TCTTAATGGA TCCCAGCTCT GTCATGGTGC TATCTATGTA TTAAGTTGGG   780
TCCTAAGTTG GGTTTTTTGT   800

        (2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 222 amino acids
            (B) TYPE. amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: GenBank
            (B) CLONE: 825605

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Glu Lys Pro Lys Leu His Tyr Ser Asn Thr Arg Gly Arg Met
 1   5   10   15
Glu Ser Ile Arg Trp Leu Leu Ala Ala Ala Gly Val Glu Phe Glu Glu
            20   25   30
Lys Phe Ile Lys Ser Ala Glu Asp Leu Asp Lys Leu Arg Asn Asp Gly
        35   40   45
Tyr Leu Met Phe Gln Gln Val Pro Met Val Glu Ile Asp Gly Met Lys
    50   55   60
Leu Val Gln Thr Arg Ala Ile Leu Asn Tyr Ile Ala Ser Lys Tyr Asn
65   70   75   80
Leu Tyr Gly Lys Asp Ile Lys Glu Lys Ala Leu Ile Asp Met Tyr Ile
                85   90   95
Glu Gly Ile Ala Asp Leu Gly Glu Met Ile Leu Leu Leu Pro Phe Thr
            100   105   110
Gln Pro Glu Glu Gln Asp Ala Lys Leu Ala Leu Ile Gln Glu Lys Thr
        115   120   125
Lys Asn Arg Tyr Phe Pro Ala Phe Glu Lys Val Leu Lys Ser His Gly
    130   135   140
Gln Asp Tyr Leu Val Gly Asn Lys Leu Ser Arg Ala Asp Ile His Leu
145   150   155   160
Val Glu Leu Leu Tyr Tyr Val Glu Glu Leu Asp Ser Ser Leu Ile Ser
                165   170   175
Ser Phe Pro Leu Leu Lys Ala Leu Lys Thr Arg Ile Ser Asn Leu Pro
            180   185   190
Thr Val Lys Lys Phe Leu Gln Pro Gly Ser Pro Arg Lys Pro Pro Met
        195   200   205
Asp Glu Lys Ser Leu Glu Glu Ser Arg Lys Ile Phe Arg Phe
    210   215   220

        (2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 222 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (vii) IMMEDIATE SOURCE:
            (A) LIBRARY: GenBank
            (B) CLONE: 159141

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      1               5                      10                         15
    Glu Ser Thr Arg Trp Leu Leu Ala Ala Ala Gly Val Glu Phe Glu Glu
                    20                      25                      30
    Lys Phe Ile Lys Ser Ala Glu Asp Leu Asp Lys Leu Arg Asn Asp Gly
                35                      40                      45
    Tyr Leu Met Phe Gln Gln Val Pro Met Val Glu Ile Asp Gly Met Lys
        50                      55                      60
    Leu Val Gln Thr Arg Ala Ile Leu Asn Tyr Ile Ala Ser Lys Tyr Asn
    65                      70                      75                      80
    Leu Tyr Gly Lys Asp Ile Lys Glu Arg Ala Leu Ile Asp Met Tyr Ile
                    85                      90                      95
    Glu Gly Ile Ala Asp Leu Gly Glu Met Ile Leu Leu Leu Pro Val Cys
                    100                     105                     110
    Pro Pro Glu Glu Lys Asp Ala Lys Leu Ala Leu Ile Lys Glu Lys Ile
                115                     120                     125
    Lys Asn Arg Tyr Phe Pro Ala Phe Glu Lys Val Leu Lys Ser His Gly
            130                     135                     140
    Gln Asp Tyr Leu Val Gly Asn Lys Leu Ser Arg Ala Asp Ile His Leu
    145                     150                     155                     160
    Val Glu Leu Leu Tyr Tyr Val Glu Glu Leu Asp Ser Ser Leu Ile Ser
                        165                     170                     175
    Ser Phe Pro Leu Leu Lys Ala Leu Lys Thr Arg Ile Ser Asn Leu Pro
                    180                     185                     190
    Thr Val Lys Lys Phe Leu Gln Pro Gly Ser Pro Arg Lys Pro Pro Met
                195                     200                     205
    Asp Glu Lys Ser Leu Glu Glu Ala Arg Lys Ile Phe Arg Phe
        210                     215                     220
```

        (2) INFORMATION FOR SEQ ID NO:5:

           (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 222 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear

           (vii) IMMEDIATE SOURCE:
               (A) LIBRARY: GenBank
               (B) CLONE: 193710

           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
    Met Ala Ala Lys Pro Lys Leu Tyr Tyr Phe Asn Gly Arg Gly Arg Met
      1               5                      10                         15
    Glu Ser Ile Arg Trp Leu Leu Ala Ala Ala Gly Val Glu Phe Glu Glu
                    20                      25                      30
    Glu Phe Leu Glu Thr Arg Glu Gln Tyr Glu Lys Met Gln Lys Asp Gly
                35                      40                      45
    His Leu Leu Phe Gly Gln Val Pro Leu Val Glu Ile Asp Gly Met Met
        50                      55                      60
    Leu Thr Gln Thr Arg Ala Ile Leu Ser Tyr Leu Ala Ala Lys Tyr Asn
    65                      70                      75                      80
    Leu Tyr Gly Lys Asp Leu Lys Glu Arg Val Arg Ile Asp Met Tyr Ala
                    85                      90                      95
    Asp Gly Thr Gln Asp Leu Met Met Met Ile Ala Val Ala Pro Phe Lys
                    100                     105                     110
    Thr Pro Lys Glu Lys Glu Glu Ser Tyr Asp Leu Ile Leu Ser Arg Ala
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145                     150                     155                     160
Leu Glu Ala Ile Leu Met Val Glu Glu Leu Ser Ala Pro Val Leu Ser
                165                     170                     175
Asp Phe Pro Leu Leu Gln Ala Phe Lys Thr Arg Ile Ser Asn Ile Pro
                180                     185                     190
Thr Ile Lys Lys Phe Leu Gln Pro Gly Ser Gln Arg Lys Pro Pro Pro
            195                     200                     205
Asp Gly Pro Tyr Val Glu Val Val Arg Ile Val Leu Lys Phe
        210                     215                     220
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